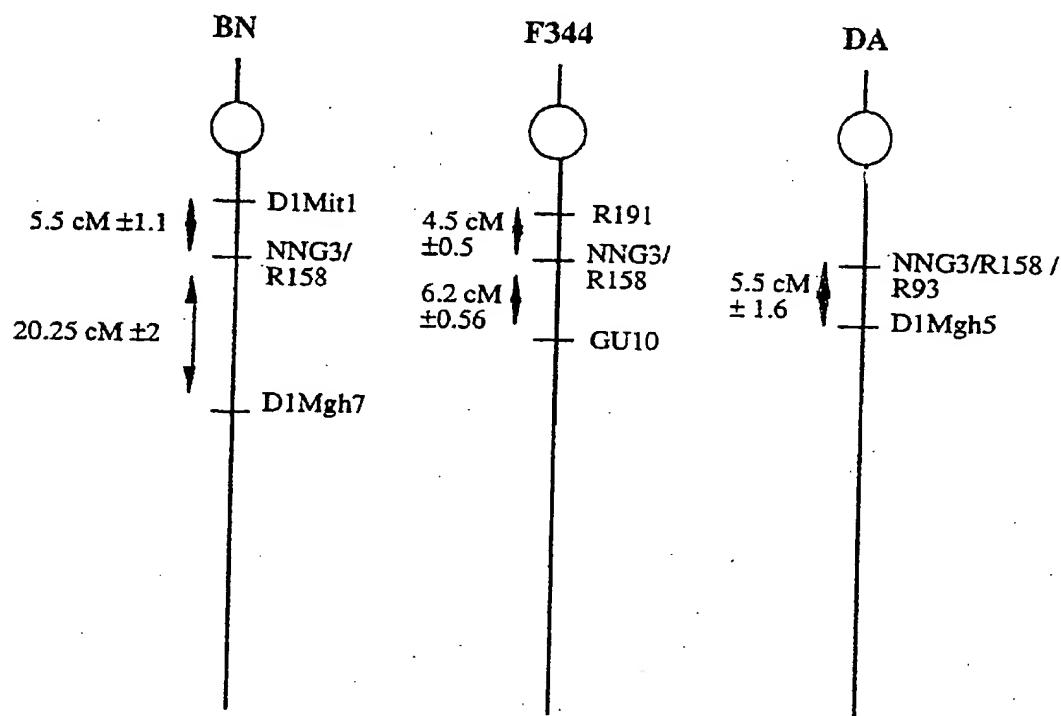


FIGURE 1

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FIGURE 2

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FIGURE 2 (CONT.)

Contig	520	530	540	550	560	570
rat mRNA	CATATTACTGTGGGTGAGGCCCGAACCTCATTCATGGACCCAATGGCTGTCTGAT					
113/114 NNG3	CATATTACTGTGGGTGAGGCCCGAACCTCATTCATGGACCCAATGGCTGTCTGAT					
113/114 AS Proof						
Contig	580	590	600	610	620	630
rat mRNA	CCCTATGTGAACTGAAGCTCATCCGGACCCCTCGAACCTGACAAAACAGAAGACAAAG					
113/114 NNG3	CCCTATGTGAACTGAAGCTCATCCGGACCCCTCGAACCTGACAAAACAGAAGACAAAG					
113/114 AS						
Contig	640	650	660	670	680	690
rat mRNA	ACCGTGAAAGCCACACTGAATCCCGTGTGGAACGAGACCTTCGTGTTCAACCTGAAGCCG					
113/114 NNG3	ACCGTGAAAGCCACACTGAATCCCGTGTGGAACGAGACCTTCGTGTTCAACCTGAAGCCG					
113/114 AS						
Contig	700	710	720	730	740	750
rat mRNA	GGGGATGTGGAGGCCGGCTCAGTGTGGAGGTGTGGGATTGGGATAGGACATCCGAAAT					
113/114 NNG3	GGGGATGTGGAGGCCGGCTCAGTGTGGAGGTGTGGGATTGGGATAGGACATCCGAAAT					
113/114 AS						
Contig	760	770	780	790	800	810
rat mRNA	GACTTCATGGGTGCCATGTCCTTGGTGTCTCAGAGCTACTCAAGGCTCTGTGGATGGA					
113/114 NNG3	GACTTCATGGGTGCCATGTCCTTGGTGTCTCAGAGCTACTCAAGGCTCTGTGGATGGA					
113/114 AS						
Contig	820	830	840	850	860	870
rat mRNA	TGGTACAAGTTACTGAACCAAGKAGGAGGGCAGTATTACAATGTACCGGTGCCGATGC					
113/114 NNG3	TGGTACAAGTTACTGAACCAAGGAGGGCAGTATTACAATGTACCGGTGCCGATGC					
113/114 AS	ACAAGTTACTGAACCAAGUAGGAGGGCAGTATTACAATGTACCGGTGCCGATGC					
	ACAAGTTACTGAACCAAGGAGGAGGGCAGTATTACAATGTACCGGTGCCGATGC					
Contig	880	890	900	910	920	930
rat mRNA	TGACAACTGCAGCCTCCCTCCAGAAGTTGAGGCCTGTAATTACCCCTTGGATTGTATGA					
113/114 NNG3	TGACAACTGCAGCCTCCCTCCAGAAGTTGAGGCCTGTAATTACCCCTTGGATTGTATGA					
113/114 AS	TGACAACTGCAGCCTCCCTCCAGAAGTTGAGGCCTGTAATTACCCCTTGGATTGTATGA					
Contig	940	950	960	970	980	990
rat mRNA	GAGAGTGGGATGGGCCCTCTCCCTCTCCATTCCCTCTCCATCCCCAGTCCCACGGA					
113/114 NNG3	GAGAGTGGGATGGGCCCTCTCCCTCTCCATTCCCTCTCCATCCCCAGTCCCACGGA					
113/114 AS	GAGAGTGGGATGGGCCCTCTCCCTCTCCATTCCCTCTCCATCCCCAGTCCCACGGA					
Contig	1000	1010	1020	1030	1040	1050
rat mRNA	CTCCAAGAGATGCTCTTCGGTGCAGCCAGGACGCCCTGCATATCTCTGACTTCAGCTT					
113/114 NNG3	CTCCAAGAGATGCTCTTCGGTGCAGCCAGGACGCCCTGCATATCTCTGACTTCAGCTT					
113/114 AS	CTCCAAGAGATGCTCTTCGGTGCAGCCAGGACGCCCTGCATATCTCTGACTTCAGCTT					
Contig	1060	1070	1080	1090	1100	1110
rat mRNA	CCTCATGGTTCTAGGGAAAGGCAGTTTGGGAAGGTGATGCTGGCAGARCGCAGAGGATC					
113/114 NNG3	CCTCATGGTTCTAGGGAAAGGCAGTTTGGGAAGGTGATGCTGGCAGAGCGCAGAGGATC					
113/114 AS	CCTCATGGTTCTAGGGAAAGGCAGTTTGGGAAGGTGATGCTGGCAGAGCGCAGAGGATC					

FIGURE 2 (CONT.)

Contig
rat mRNA
113/114 NNG3
113/114 AS

1120 1130 1140 1150 1160 1170

CGATGAAC TCTATGCCATCAAGATNCTGAAAAAAGACGTCATTGTCCAGGATGATGATGT
CGATGAAC TCTATGCCATCAAGATACTGAAAAAAGACGTCATTGTCCAGGATGATGATGT
CGATGAAC TCTATGCCATCAAGATACTGAAAAAAG
CGATGAAC TCTATGCCATCAAGATNCTGAAAAAAG

Contig
rat mRNA
113/114 NNG3
113/114 AS

1180 1190 1200 1210 1220 1230

AGACTGCACCCCTGTGGAGAACGCGTGTGGCATTGGGAGGCCGAGGTCCCTGGAGGCCG
AGACTGCACCCCTGTGGAGAACGCGTGTGGCATTGGGAGGCCGAGGTCCCTGGAGGCCG

Contig
rat mRNA
113/114 NNG3
113/114 AS

1240 1250 1260 1270 1280 1290

GCCACACTTCTCACACAAC TTCA TTCCACCTTCA GACTCCGACCGCCTGTATTTGT
GCCACACTTCTCACACAAC TTCA TTCCACCTTCA GACTCCGACCGCCTGTATTTGT

Contig
rat mRNA
113/114 NNG3
113/114 AS

1300 1310 1320 1330 1340 1350

GATGGAGTACGTCACTGGGGCGATTTAATGTACCA CATT CAGCAACTGGCAAGTTAA
GATGGAGTACGTCACTGGGGCGATTTAATGTACCA CATT CAGCAACTGGCAAGTTAA

Contig
rat mRNA
113/114 NNG3
113/114 AS

1360 1370 1380 1390 1400 1410

GGAGCCCCACGCAGCATTCTATGCCCGGAAATGCCATAGGCCCTTTCTTCACAA
GGAGCCCCACGCAGCATTCTATGCCCGGAAATGCCATAGGCCCTTTCTTCACAA

Contig
rat mRNA
113/114 NNG3
113/114 AS

1420 1430 1440 1450 1460 1470

CCAGGGCATCATCACAGGGACCTCAAGTTGGATAATGTGATGCTGGATGCTGAAGGACA
CCAGGGCATCATCACAGGGACCTCAAGTTGGATAATGTGATGCTGGATGCTGAAGGACA

Contig
rat mRNA
113/114 NNG3
113/114 AS

1480 1490 1500 1510 1520 1530

CATCAAGATCACAGACTTCGGCATGTGTAAAGAGAAATGTCTTCCCTGGGTCCACAACCCG
CATCAAGATCACAGACTTCGGCATGTGTAAAGAGAAATGTCTTCCCTGGGTCCACAACCCG

Contig
rat mRNA
113/114 NNG3
113/114 AS

1540 1550 1560 1570 1580 1590

CACCTTCTGTGGGACCCCAGACTACATAGCACCTGAGATCATTGCCCTATCAGCCCTATGG
CACCTTCTGTGGGACCCCAGACTACATAGCACCTGAGATCATTGCCCTATCAGCCCTATGG

Contig
rat mRNA
113/114 NNG3
113/114 AS

1600 1610 1620 1630 1640 1650

GAAGTCTGTCGACTGGTGGCCTTGGAGTCCTGCTGTATGAGATGTTGGCAGGACAGCC
GAAGTCTGTCGACTGGTGGCCTTGGAGTCCTGCTGTATGAGATGTTGGCAGGACAGCC

Contig
rat mRNA
113/114 NNG3
113/114 AS

1660 1670 1680 1690 1700 1710

ACCCCTTGATGGGGAAAGATGAGGGAGGAGCTTTCAAGCCATCATGGAACAAACTGTCAC
ACCCCTTGATGGGGAAAGATGAGGGAGGAGCTTTCAAGCCATCATGGAACAAACTGTCAC

Contig
rat mRNA
113/114 NNG3
113/114 AS

1720 1730 1740 1750 1760 1770

CTATCCCAAGTCACCTTCCGGAAAGCTGTGGCCATCTGCAAGGGTTCTGACCAAGCA
CTATCCCAAGTCACCTTCCGGAAAGCTGTGGCCATCTGCAAGGGTTCTGACCAAGCA

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FIGURE 2 (CONT)

1780 1790 1800 1810 1820 1830
 Contig
 rat mRNA
 113/114 NNG3
 113/114 AS
 CCCAGGAAAGCGCCTGGGCTCAGGGCCAGATGGGGAAACCCACCATCCGGGCTCATGGCTT
 CCCAGGAAAGCGCCTGGGCTCAGGGCCAGATGGGGAAACCCACCATCCGGGCTCATGGCTT

1840 1850 1860 1870 1880 1890
 Contig
 rat mRNA
 113/114 NNG3
 113/114 AS
 TTTCCGTTGGATCGATTGGGAGAGGTTGGAGAGACTGGAAATTGCGCCTCCTTTAGACC
 TTTCCGTTGGATCGATTGGGAGAGGTTGGAGAGACTGGAAATTGCGCCTCCTTTAGACC

1900 1910 1920 1930 1940 1950
 Contig
 rat mRNA
 113/114 NNG3
 113/114 AS
 ACGTCCGTGTGGCCCGCAGCGGGGAAAACCTTACAAGTTCTCACGCAGGGCAGCGCCAGC
 ACGTCCGTGTGGCCCGCAGCGGGGAAAACCTTACAAGTTCTCACGCAGGGCAGCGCCAGC

1960 1970 1980 1990 2000 2010
 Contig
 rat mRNA
 113/114 NNG3
 113/114 AS
 CTTGACCCCGCCAGACCGCTTGGTCTAGCCAGCATCGACCAAGCTGATTTCAAGGGCTT
 CTTGACCCCGCCAGACCGCTTGGTCTAGCCAGCATCGACCAAGCTGATTTCAAGGGCTT

2020 2030 2040 2050 2060 2070
 Contig
 rat mRNA
 113/114 NNG3
 113/114 AS
 TACTTATGTGAACCCGGACTTCGTGCACCCAGATGCCCGCAGCCCCACAAGCCCTGTGCC
 TACTTATGTGAACCCGGACTTCGTGCACCCAGATGCCCGCAGCCCCACAAGCCCTGTGCC

2080 2090 2100 2110 2120 2130
 Contig
 rat mRNA
 113/114 NNG3
 113/114 AS
 TGTGCCGTCATGTAATCTCATCTGCTGCCCTAGGTGTTCCAGTGCTCCCTCCGCCAA
 TGTGCCGTCATGTAATCTCATCTGCTGCCCTAGGTGTTCCAGTGCTCCCTCCGCCAA
Stop Codon

2140 2150 2160 2170 2180 2190
 Contig
 rat mRNA
 113/114 NNG3
 113/114 AS
 GTTGGCTGTAACTCCATCCACCCCCATCCCGCCTCTAGTCGAATTAGGTCTCTTA
 GTTGGCTGTAACTCCATCCACCCCCATCCCGCCTCTAGTCGAATTAGGTCTCTTA

2200 2210 2220 2230 2240 2250
 Contig
 rat mRNA
 113/114 NNG3
 113/114 AS
 AACCAACCCAAACCTCTGGCCTCTTCACGCCCAAGTGGGTTCTAGACGCTGTTCCCC
 AACCAACCCAAACCTCTGGCCTCTTCACGCCCAAGTGGGTTCTAGACGCTGTTCCCC

2260 2270 2280 2290 2300 2310
 Contig
 rat mRNA
 113/114 NNG3
 113/114 AS
 AGCATTGCTGGCATTAAACTCAAACAGTCTCTAGAGCCTTCTGTGTTCTAGATTG
 AGCATTGCTGGCATTAAACTCAAACAGTCTCTAGAGCCTTCTGTGTTCTAGATTG

2320 2330 2340 2350 2360 2370
 Contig
 rat mRNA
 113/114 NNG3
 113/114 AS
 TTGTGCTGAGCCCTGGTTCCCCACCCCCAACATCTGGATGCTGTTCCAACCTTCCC
 TTGTGCTGAGCCCTGGTTCCCCACCCCCAACATCTGGATGCTGTTCCAACCTTCCC

2380 2390 2400 2410 2420 2430
 Contig
 rat mRNA
 113/114 NNG3
 113/114 AS
 AGAAACCCACTCCGTGTGGGTTCTAGACTCTATCTGGTAGTTTATGCCCTCTCT
 AGAAACCCACTCCGTGTGGGTTCTAGACTCTATCTGGTAGTTTATGCCCTCTCT

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FIGURE 2 (CONT)

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FIGURE 3

-141

TGCTTTC

-134 TGCCCTGCGCTGCGCACCGTTAGTGCCTGCCCTGCTCCGATCTCAGAGTCTGCCAGTGCCC
-67 CTATGCCGTCCACCTGTTCCCTCAGAAAAAGGCCAGCTCGTGA
TCCCTGCGTTCCCTGGGGCCStart Ala Gly Leu Gly Pro Gly Gly Asp Ser Glu Gly Pro Arg Pro 17
1 ATG GCG GGT CTG GGT CCT GGC GGG GGC GAC TCA GAA GGG GGA CCC CGA CCCLeu Phe Cys Arg Lys Gly Ala Leu Arg Gln Lys Val Val His Glu Val Lys 34
52 CTG TTT TGC AGA AAG GGG GCG CTG AGG CAG AAG GTG GTC CAC GAG GTG AAGSer His Lys Phe Thr Ala Arg Phe Phe Lys Gln Pro Thr Phe Cys Ser His 51
103 AGC CAC AAG TTC ACC GCT CGT TTC AAG CAG CCA ACC TTC TGC AGT CACCys Thr Asp Phe Ile Trp Gly Ile Gly Lys Gln Gly Leu Gln Cys Gln Val 68
154 TGT ACC GAC TTC ATC TGG GGC ATT GGA AAG CAG GGC CTG CAA TGT CAA GTCCys Ser Phe Val Val His Arg Arg Cys His Glu Phe Val Thr Phe Glu Cys 85
205 TGC AGC TTT GTG GTT CAC CGC CGA TGC CAC GAA TTT GTG ACC TTC GAG TGTPro Gly Ala Gly Lys Gly Pro Gln Thr Asp Asp Pro Arg Asn Lys His Lys 102
256 CCA GGC GCT GGA AAG GGC CCC CAG ACG GAC CCT CGC AAC AAG CAC AAGPhe Arg Leu His Ser Tyr Ser Ser Pro Thr Phe Cys Asp His Cys Gly Ser 119
307 TTC CGT CTG CAC AGC TAC AGC AGT CCC ACC TTC TGC GAC CAC TGT GGT TCCLeu Leu Tyr Gly Leu Val His Gln Gly Met Lys Cys Ser Cys Cys Glu Met 136
358 CTC CTC TAC GGG CTG GTG CAC CAG GGC ATG AAA TGT TCC TGT TGC GAA ATGAsn Val His Arg Arg Cys Val Arg Ser Val Pro Ser Leu Cys Gly Val Asp 153
409 AAT GTG CAC CGA CGC TGT GTG CGC AGC GTG CCC TCC CTT TGC GGC GTG GACHis Thr Glu Arg Arg Gly Arg Leu Gln Leu Glu Ile Arg Ala Pro Thr Ser 170
460 CAT ACA GAG CGC CGT GGA CGT CTG CAA CTG GAA ATC CGG GCT CCC ACA TCAAsp Glu Ile His Ile Thr Val Gly Glu Ala Arg Asn Leu Ile Pro Met Asp 187
511 GAT GAG ATC CAT ATT ACT GTG GGT GAG GCC CGG AAC CTC ATT CCT ATG GACPro Asn Gly Leu Ser Asp Pro Tyr Val Lys Leu Lys Leu Ile Pro Asp Pro 204
562 CCC AAT GGC CTG TCT GAT CCC TAT GTG AAA CTG AAG CTC ATC CCG GAC CCTArg Asn Leu Thr Lys Gln Lys Thr Lys Thr Val Lys Ala Thr Leu Asn Pro 221
613 CGG AAC CTG ACA AAA CAG AAG ACA AAG ACC GTG AAA GCC ACA CTG AAT CCCVal Trp Asn Glu Thr Phe Val Phe Asn Leu Lys Pro Gly Asp Val Glu Arg 238
664 GTG TGG AAC GAG ACC TTC GTG TTC AAC CTG AAG CCG GGG GAT GTG GAG CGCArg Leu Ser Val Glu Val Trp Asp Trp Asp Arg Thr Ser Arg Asn Asp Phe 255
715 CGG CTC AGT GTG GAG GTG TGG GAT TGG GAT AGG ACA TCC CGA AAT GAC TTCMet Gly Ala Met Ser Phe Gly Val Ser Glu Leu Leu Lys Ala Pro Val Asp 272
766 ATG GGT GCC ATG TCC TTT GGT GTC TCA GAG CTA CTC AAG GCT CCT GTG GATGly Trp Tyr Lys Leu Leu Asn Gln Glu Glu Gly Glu Tyr Tyr Asn Val Pro 289
817 GGA TGG TAC AAG TTA CTG AAC CAG GAG GAG GGC GAG TAT TAC AAT GTA CCG
TAG

Mutant NNG3 STOP

Val Ala Asp Ala Asp Asn Cys Ser Leu Leu Gln Lys Phe Glu Ala Cys Asn 306
868 GTG GCC GAT GCT GAC AAC TGC AGC CTC CTC CAG AAG TTT GAG GCC TGT AATTyr Pro Leu Glu Leu Tyr Glu Arg Val Arg Met Gly Pro Ser Ser Ser Pro 323
919 TAC CCC TTG GAA TTG TAT GAG AGA GTG CGG ATG GGC CCC TCT TCC TCT CCCIle Pro Ser Pro Ser Pro Ser Pro Thr Asp Ser Lys Arg Cys Phe Phe Gly 340
970 ATT CCT TCT CCA TCC CCC AGT CCC ACG GAC TCC AAG AGA TGC TTC GGT

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FIGURE 3 (CONT)

Ala Ser Pro Gly Arg Leu His Ile Ser Asp Phe Ser Phe Leu Met Val Leu 357
 1021 GCC AGC CCA GGA CGC CTG CAT ATC TCT GAC TTC AGC TTC CTC ATG GTT CTA

 Gly Lys Gly Ser Phe Gly Lys Val Met Leu Ala Glu Arg Arg Gly Ser Asp 374
 1072 GGG AAA GGC AGT TTT GGG AAG GTG ATG CTG GCA GAG CGC AGA GGA TCC GAT

 Glu Leu Tyr Ala Ile Lys Ile Leu Lys Lys Asp Val Ile Val Gln Asp Asp 391
 1123 GAA CTC TAT GCC ATC AAG ATA CTG AAA AAA GAC GTC ATT GTC CAG GAT GAT

 Asp Val Asp Cys Thr Leu Val Glu Lys Arg Val Leu Ala Leu Gly Gly Arg 408
 1174 GAT GTA GAC TGC ACC CTT GTG GAG AAG CGT GTG CTG GCA TTG GGA GGC CGA

 Gly Pro Gly Gly Arg Pro His Phe Leu Thr Gln Leu His Ser Thr Phe Gln 425
 1225 GGT CCT GGA GGC CGG CCA CAC TTT CTC ACA CAA CTT CAT TCC ACC TTT CAG

 Thr Pro Asp Arg Leu Tyr Phe Val Met Glu Tyr Val Thr Gly Gly Asp Leu 442
 1276 ACT CCG GAC CGC CTG TAT TTT GTG ATG GAG TAC GTC ACT GGG GGC GAT TTA

 Met Tyr His Ile Gln Gln Leu Gly Lys Phe Lys Glu Pro His Ala Ala Phe 459
 1327 ATG TAC CAC ATT CAG CAA CTG GGC AAG TTT AAG GAG CCC CAC GCA GCA TTC

 Tyr Ala Ala Glu Ile Ala Ile Gly Leu Phe Phe Leu His Asn Gln Gly Ile 476
 1378 TAT GCC GCG GAA ATC GCC ATA GGC CTC TTC CTT CAC AAC CAG GGC ATC

 Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Met Leu Asp Ala Glu Gly His 493
 1429 ATC TAC AGG GAC CTC AAG TTG GAT AAT GTG ATG CTG GAT GCT GAA GGA CAC

 Ile Lys Ile Thr Asp Phe Gly Met Cys Lys Glu Asn Val Phe Pro Gly Ser 510
 1480 ATC AAG ATC ACA GAC TTC GGC ATG TGT AAA GAG AAT GTC TTC CCT GGG TCC

 Thr Thr Arg Thr Phe Cys Gly Thr Pro Asp Tyr Ile Ala Pro Glu Ile Ile 527
 1531 ACA ACC CGC ACC TTC TGT GGG ACC CCA GAC TAC ATA GCA CCT GAG ATC ATT

 Ala Tyr Gln Pro Tyr Gly Lys Ser Val Asp Trp Trp Ser Phe Gly Val Leu 544
 1582 GCC TAT CAG CCC TAT GGG AAG TCT GTC GAC TGG TGG TCC TTT GGA GTC CTG

 Leu Tyr Glu Met Leu Ala Gly Gln Pro Pro Phe Asp Gly Glu Asp Glu Glu 561
 1633 CTG TAT GAG ATG TTG GCA GGA CAG CCA CCC TTT GAT GGG GAA GAT GAG GAG

 Glu Leu Phe Gln Ala Ile Met Glu Gln Thr Val Thr Tyr Pro Lys Ser Leu 578
 1684 GAG CTG TTT CAA GCC ATC ATG GAA CAA ACT GTC ACC TAT CCC AAG TCA CTT

 Ser Arg Glu Ala Val Ala Ile Cys Lys Gly Phe Leu Thr Lys His Pro Gly 595
 1735 TCC CGG GAA GCT GTG GCC ATC TGC AAG GGG TTC CTG ACC AAG CAC CCA GGA

 Lys Arg Leu Gly Ser Gly Pro Asp Gly Glu Pro Thr Ile Arg Ala His Gly 612
 1786 AAG CGC CTG GGC TCA GGG CCA GAT GGG GAA CCC ACC ATC CGG GCT CAT GGC

 Phe Phe Arg Trp Ile Asp Trp Glu Arg Leu Glu Arg Leu Glu Ile Ala Pro 629
 1837 TTT TTC CGT TGG ATC GAT TGG GAG AGG TTG GAG AGA CTG GAA ATT GCG CCT

 Pro Phe Arg Pro Arg Pro Cys Gly Arg Ser Gly Glu Asn Phe Asp Lys Phe 646
 1888 CCT TTT AGA CCA CGT CCG TGT GGC CGC AGC GGC GAA AAC TTT GAC AAG TTC

 Phe Thr Arg Ala Ala Pro Ala Leu Thr Pro Pro Asp Arg Leu Val Leu Ala 663
 1939 TTC ACG CGG GCA GCG CCA GCC TTG ACC CCG CCA GAC CGC TTG GTC CTA GCC

 Ser Ile Asp Gln Ala Asp Phe Gln Gly Phe Thr Tyr Val Asn Pro Asp Phe 680
 1990 AGC ATC GAC CAA GCT GAT TTC CAG GGC TTT ACT TAT GTG AAC CCG GAC TTC

 Val His Pro Asp Ala Arg Ser Pro Thr Ser Pro Val Pro Val Pro Val Met 697
 2014 GTG CAC CCA GAT GCC CGC AGC CCC ACA AGC CCT GTG CCT GTG CCC GTC ATG

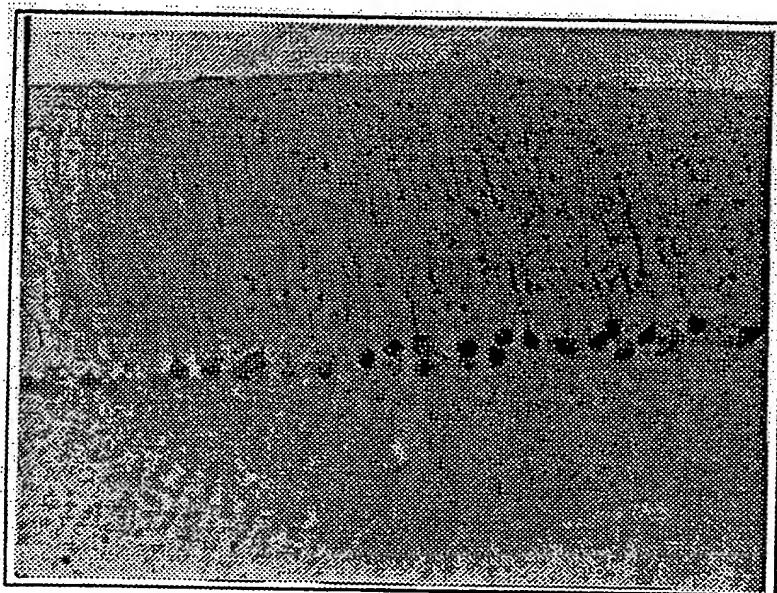
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FIGURE 3 (CONT)

stop

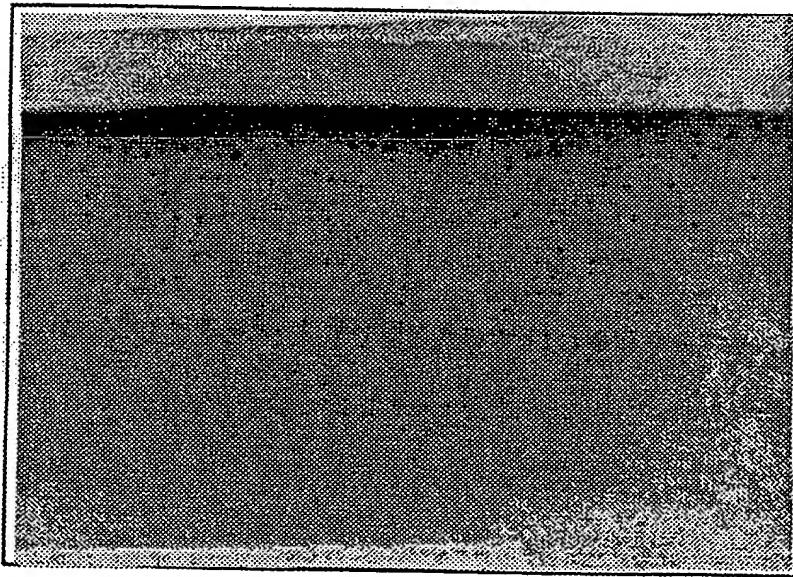
2092 TAA TCTCATCTGCTGCCGCTAGGTGTTCCCAGTGCTCCCTCCGCAAGTTGGCTGTAACCTCCCATC
2158 CACCCCCCATCCCCGCCCTAGTCCGAATTTAGGTCTCTTAAACCACCCAAACCTCTGGCCTTTTC
2225 ACGCGCCCCAAGTGGGTTCTAGACGCTTTCCCGAGCATTGCTGGCATTTAAACTTCAAACAGTCT
2292 CTAGAGCCTTCTGTGTTCTAGATTGTTGTGCTGAGCCCTGGTTTTCCCCACCCCCAACATCTGG
2359 ATGCTGTTCCAACCTCTCCAGAAAACCCCACCTCCGTGTTGGGTTCTAGACTCTATCTGGTAGTTT
2426 ATGCTCTCTCTCCCTAGACACGTTGGAGAAAATAGTCTCATGAGATTGCTGCTCCAGACTAAAG
2493 ATTCCAGATCAGCTCTCTGCATCCTCAAGGCCCCCTACCTCCACTTCAGTTGAGAATTAAAGTG
2560 GGAGGCTGGGCTCCGTGTTCCAGGCCACCTCCCTTCATGTTCTGGGATTCTGGCATGCAACGGAG
2627 GATTCTCTCCCCGACTTTCTCAGTCAGCTTTGTTCTAGATTGTTCCAGAACCCCTCACTGCTCA
2694 CCTGCCCCGTGCATGGCTCAGCCTTGGTCGGAATCACACACACACACACACACACACACA
2761 CA
2828 CCCACGCCCTTCTTATCCTCTCCACCCAGACACAGCTGCTGGAGAATAATTG

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FIGURE 4**A**

← Granule cell layer

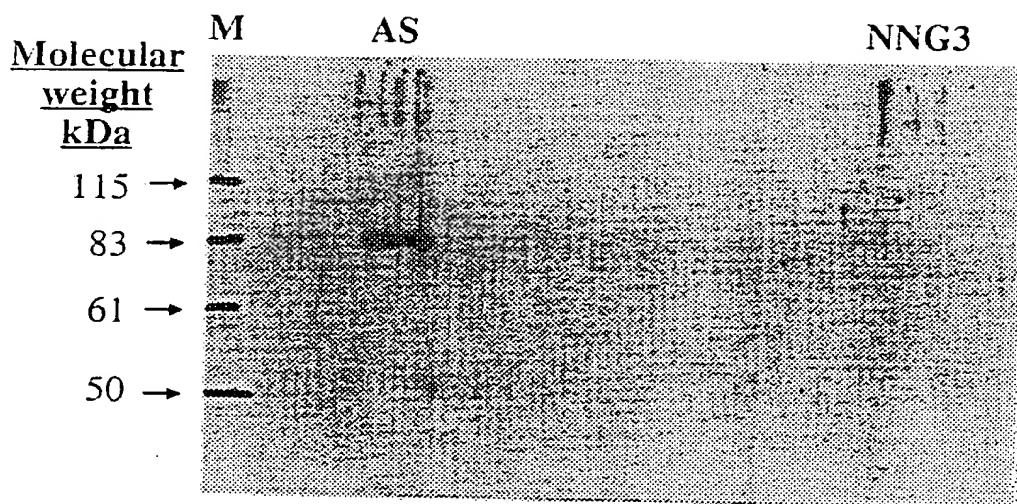
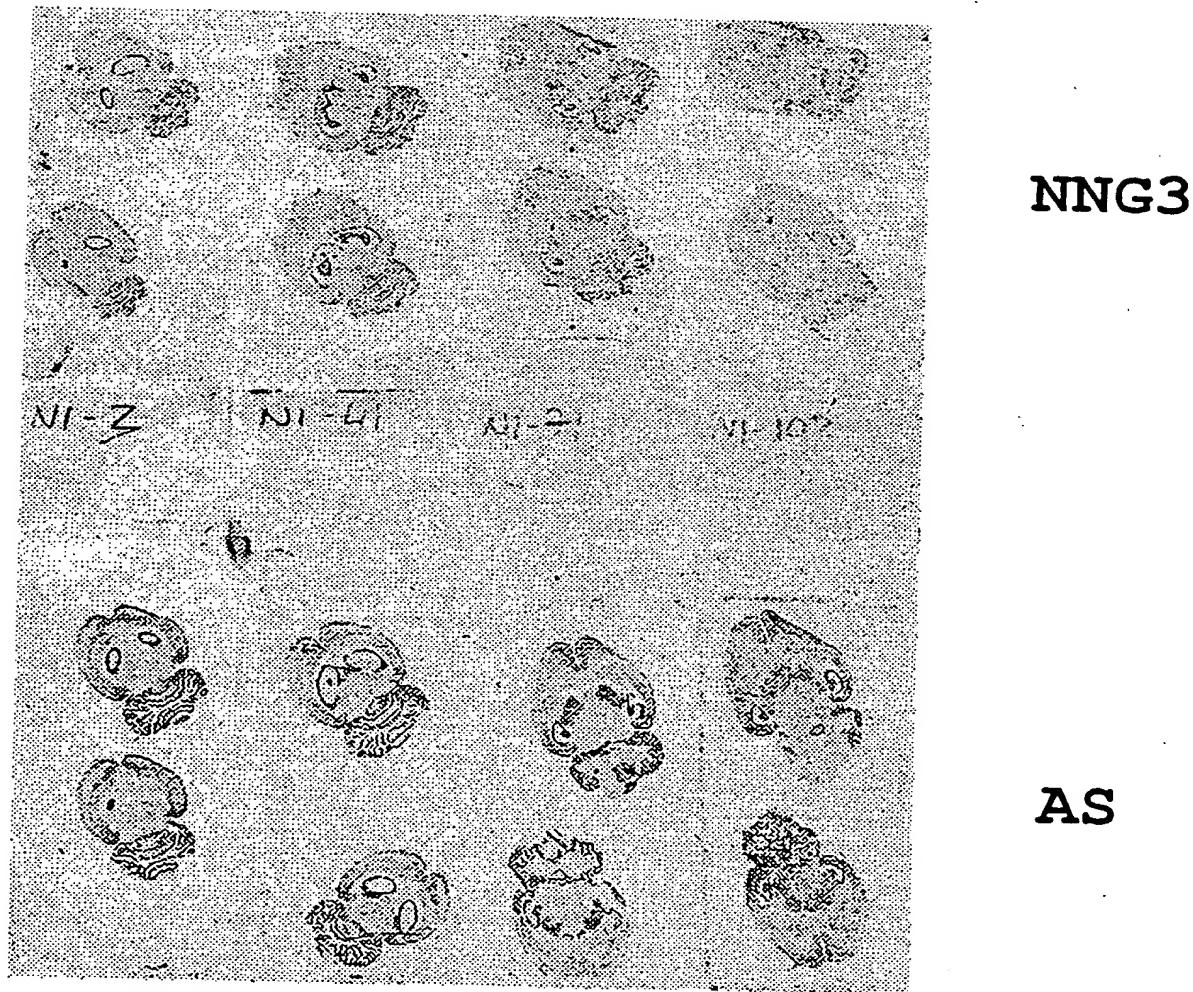
← Purkinje cell layer

B

← Granule cell layer

← Purkinje cell layer

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FIGURE 5FIGURE 6

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FIGURE 7

Start codon

```

-140      -130      -120      -110      -100      -90      -80      -70
|         |         |         |         |         |         |         |
TGCTTTCTGCCCTGCGCTGCGCACCGTTAGTGCCTGCCCCCTGCTCCGATCTCAGAGTCTGCGGAGTGCCCCCTA
.....  

.....  

TCCTTCCGATCTCAGAGTCTGCGGAGTGCCCCCTA

-60      -50      -40      -30      -20      -10      1      10
|         |         |         |         |         |         |         |
TCGCCGTCCACCTGTTCTCAGAAAAAGGCCAGCTCGTATCCCTGCTGCGTTCTGGGGCATGGCGGGTCTGG
.....  

.....  

TCGCCGTCCACCTGTTCTCAGAAAAAGGCCAGCTCGTATCCCTGCTGCGTTCTGGGGCATGGCGGGTCTGG

20      30      40      50      60      70      80      90
|         |         |         |         |         |         |         |
GTCCCTGGGGGGGGGACTCAGAAGGGGGACCCCTGTTTGCAGAAAGGGGGCGTGAGGCAGAAGGTGGTC
.....  

.....  

GTCCCTGGGGGGGGGACTCAGAAGGGGGACCCCTGTTTGCAGAAAGGGGGCGTGAGGCAGAAGGTGGTC

100     110     120     130     140     150     160
|         |         |         |         |         |         |
CACGAGGTGAAGAGGCCACAAGTTACCGCTCGTTCTCAAGCAGCCAACCTCTGCAGTCAGTACGTACCGACTTCAT
.....  

.....  

CACGAGGTGAAGAGGCCACAAGTTACCGCTCGTTCTCAAGCAGCCAACCTCTGCAGTCAGTACGTACCGACTTCAT

170     180     190     200     210     220     230     240
|         |         |         |         |         |         |         |
CTGGGGCATGGAAAGCAGGGCTGCAATGTCAGTCTGCAGCTTGTGGTTCACCGCCGATGCCACGAATTGTGA
.....  

.....  

CTGGGGCATGGAAAGCAGGGCTGCAATGTCAGGTCTGCAGCTTGTGGTTCACCGCCGATGCCACGAATTGTGA

250     260     270     280     290     300     310     320
|         |         |         |         |         |         |         |
CCTTCGAGTGTCCAGGCCTGGAAAGGGCCCCAGACGGACGACCCCTCGAACAGCACAGAACAGTCCGTCTGCACAGC
.....  

.....  

CCTTCGAGTGTCCAGGCCTGGAAAGGGCCCCAGACGGACGACCCCTCGAACAGCACAGAACAGTCCGTCTGCACAGC

330     340     350     360     370     380     390
|         |         |         |         |         |         |
TACAGCAGTCCCACCTCTGCGACCACTGTGGTCCCTCCTACGGCTGGTGCACCAGGGATGAAATGTTCTG
.....  

.....  

TACAGCAGTCCCACCTCTGCGACCACTGTGGTCCCTCCTACGGCTGGTGCACCAGGGATGAAATGTTCTG

400     410     420     430     440     450     460     470
|         |         |         |         |         |         |
TTGCGAAATGAATGTCACCGACGCTGTGTGCGCAGCGTGCCTCCCTTGCGGGTGGACCATAAGAGCGCCGTG
.....  

.....  

TTGCGAAATGAATGTCACCGACGCTGTGTGCGCAGCGTGCCTCCCTTGCGGGTGGACCATAAGAGCGCCGTG

480     490     500     510     520     530     540     550
|         |         |         |         |         |         |
GACGTCTGCAACTGGAAATCCGGGCTCCACATCAGATGAGATCCATATTACTGTGGGTGAGGCCCGAACCTCATT
.....  

.....  

GACGTCTGCAACTGGAAATCCGGGCTCCACATCAGATGAGATCCATATTACTGTGGGTGAGGCCCGAACCTCATT

560     570     580     590     600     610     620
|         |         |         |         |         |         |
CCTATGGACCCAATGGCTGTCTGATCCCTATGTGAAACTGAAGCTCATCCCGAACCTCGGAACCTGACAAAACA
.....  

.....  

CCTATGGACCCAATGGCTGTCTGATCCCTATGTGAAACTGAAGCTCATCCCGAACCTCGGAACCTGACAAAACA

630     640     650     660     670     680     690     700
|         |         |         |         |         |         |
GAAGACAAAGACCGTGAAAGCCACACTGAATCCCGTGTGGAACGAGACCTTCGTGTTCAACCTGAAGCCGGGGATG
.....  

.....  

GAAGACAAAGACCGTGAAAGCCACACTGAATCCCGTGTGGAACGAGACCTTCGTGTTCAACCTGAAGCCGGGGATG

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FIGURE 7 (CONT)

710 720 730 740 750 760 770 780
 | | | | | | | |
 TGGAGCGCCGGCTCAGTGTGGAGGTGTGGATTGGGATAGGACATCCGAAATGACTTCATGGGTGCCATGTCCTTT

 TGGAGCGCCGGCTCAGTGTGGAGGTGTGGATTGGGATAGGACATCCGAAATGACTTCATGGGTGCCATGTCCTTT

 790 800 810 820 830 840 850 860
 | | | | | | | |
 GGTGTCTCAGAGCTACTCAAGGCTCTGTGGATGGATGGTACAAGTTACTGAACCAGGAGGAGGGCGAGTATTACAA

 GGTGTCTCAGAGCTACTCAAGGCTCTGTGGATGGATGGTACAAGTTACTGAACCAGGAGGAGGGCGAGTATTACAA

 870 880 890 900 910 920 930
 | | | | | | |
 TGTACCGGTGGCGATGCTGACAAC TG CAGCCTCCCTCCAGAAGTTGAGGCCTGTAATTACCCCTTGGAAATTGTATG

 TGTACCGGTGGCGATGCTGACAAC TG CAGCCTCCCTCCAGAAGTTGAGGCCTGTAATTACCCCTTGGAAATTGTATG

 940 950 960 970 980 990 1000 1010
 | | | | | | | |
 AGAGAGTGGGATGGGCCCTTCTCTCTCCATTCTCCATCCCCCAGTCCCACGGACTCCAAGAGATGCTTC

 AGAGAGTGGGATGGGCCCTTCTCTCTCCATTCTCCATCCCCCAGTCCCACGGACTCCAAGAGATGCTTC

 1020 1030 1040 1050 1060 1070 1080 1090
 | | | | | | | |
 TTCGGTGCCAGCCCAGGACGCCCTGCATATCTCTGACTTCAGCTTCCTCATGGTCTAGGGAAAGGCAGTTTGGGAA

 TTCGGTGCCAGCCCAGGACGCCCTGCATATCTCTGACTTCAGCTTCCTCATGGTCTAGGGAAAGGCAGTTTGGGAA

 1100 1110 1120 1130 1140 1150 1160
 | | | | | | |
 GGTGATGCTGGCAGAGCGCAGAGGATCCGATGAAC TCTATGCCATCAAGATACTGAAAAAGACGTCATTGTCCAGG

 GGTGATGCTGGCAGAGCGCAGAGGATCCGATGAAC TCTATGCCATCAAGATACTGAAAAAGACGTCATTGTCCAGG

 1170 1180 1190 1200 1210 1220 1230 1240
 | | | | | | | |
 ATGATGATGTAGACTGCACCCCTTGTGGAGAAGCGTGTGCTGGCATTGGGAGGCCAGGTCTGGAGGCCGGCACAC

 ATGATGATGTAGACTGCACCCCTTGTGGAGAAGCGTGTGCTGGCATTGGGAGGCCAGGTCTGGAGGCCGGCACAC

 1250 1260 1270 1280 1290 1300 1310 1320
 | | | | | | | |
 TTTCTCACACAAC TTCA TCCACCTT CAGACTCCGGACC GCGCTGTATTGTGATGGAGTACGTCACTGGGGCGA

 TTTCTCACACAAC TTCA TCCACCTT CAGACTCCGGACC GCGCTGTATTGTGATGGAGTACGTCACTGGGGCGA

 1330 1340 1350 1360 1370 1380 1390
 | | | | | | |
 TTTAATGTACCA CATT CAGCAACTGGCAAGTTAAGGAGCCCACGCAGCATTCTATGCCCGGAAATGCCATAG

 TTTAATGTACCA CATT CAGCAACTGGCAAGTTAAGGAGCCCACGCAGCATTCTATGCCCGGAAATGCCATAG

 1400 1410 1420 1430 1440 1450 1460 1470
 | | | | | | | |
 GCCTCTTCTT CTT CACA ACCAGGGCATCATCTACAGGGACCTCAAGTTGATAATGTGATGCTGGATGCTGAAGGA

 GCCTCTTCTT CTT CACA ACCAGGGCATCATCTACAGGGACCTCAAGTTGATAATGTGATGCTGGATGCTGAAGGA

 1480 1490 1500 1510 1520 1530 1540 1550
 | | | | | | | |
 CACATCAAGATCACAGACTTCGGCATGTGTAAAGAGAATGTCTCCCTGGGTCCACAACCCGCACCTCTGTGGGAC

 CACATCAAGATCACAGACTTCGGCATGTGTAAAGAGAATGTCTCCCTGGGTCCACAACCCGCACCTCTGTGGGAC

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FIGURE 7 (CONT)

1560 1570 1580 1590 1600 1610 1620 1630
 CCCAGACTACATAGCACCTGAGATCATTGCCATGCCCTATGGGAAGTCTGTCAGTGGTGGCCTTGGAGTCC
 CCCAGACTACATAGCACCTGAGATCATTGCCATGCCCTATGGGAAGTCTGTCAGTGGTGGCCTTGGAGTCC

 1640 1650 1660 1670 1680 1690 1700
 TGCTGTATGAGATGTTGGCAGGACAGCCACCCCTTGATGGGAAGATGAGGAGGAGCTGTTCAAGCCATCATGGAA
 TGCTGTATGAGATGTTGGCAGGACAGCCACCCCTTGATGGGAAGATGAGGAGGAGCTGTTCAAGCCATCATGGAA

 1710 1720 1730 1740 1750 1760 1770 1780
 CAAACTGTCACCTATCCCAAGTCACCTTCCGGGAAGCTGTCAGGCTATGCCAAGGGGTTCCGTGACCAAGCACCAGG
 CAAACTGTCACCTATCCCAAGTCACCTTCCGGGAAGCTGTCAGGCTATGCCAAGGGGTTCCGTGACCAAGCACCAGG

 1790 1800 1810 1820 1830 1840 1850 1860
 AAAGCGCTGGGCTCAGGGCCAGATGGGAACCCACCATCCGGCTCATGGCTTTCCGGATCGATTGGGAGA
 AAAGCGCTGGGCTCAGGGCCAGATGGGAACCCACCATCCGGCTCATGGCTTTCCGGATCGATTGGGAGA

 1870 1880 1890 1900 1910 1920 1930
 GGTTGGAGAGACTGGAAATTGCGCCTCTTTAGACCACGTCCTGTCAGGGCGAGCGGGAAAACCTTGACAAGTTC
 GGTTGGAGAGACTGGAAATTGCGCCTCTTTAGACCACGTCCTGTCAGGGCGAGCGGGAAAACCTTGACAAGTTC

 1940 1950 1960 1970 1980 1990 2000 2010
 TTACCGGGCAGCGCCAGCCTTGACCCGCCAGACCGCTGGCTCTAGCCAGCATCGACCAAGCTGATTCCAGGG
 TTACCGGGCAGCGCCAGCCTTGACCCGCCAGACCGCTGGCTCTAGCCAGCATCGACCAAGCTGATTCCAGGG

 2020 2030 2040 2050 2060 2070 2080 2090
 CTTTACTTATGTGAACCCGGACTTCGTGCACCCAGATGCCCGAGCCCCACAAGCCCTGTGCCTGTGCCGTGATG
 CTTTACTTATGTGAACCCGGACTTCGTGCACCCAGATGCCCGAGCCCCACAAGCCCTGTGCCTGTGCCGTGATG

 2100 2110 2120 2130 2140 2150 2160 2170
 TAATCTCATCTGCTGCCGCTAGGTGTTCCAGTGCCTCCCTCCGCCAAGTGGCTGTAACCTCCATCCACCCCATCCC
 TAATCTCATCTGCTGCCGCTAGGTGTTCCAGTGCCTCCCTCCGCCAAGTGGCTGTAACCTCCATCCACCCCATCCC
Stop Codon

 2180 2190 2200 2210 2220 2230 2240
 CGCCTCTAGTCGAATTAGGTCTCTAAACCAACCCACCTCTGGCCTTTCACGCGCCCCAAGTGGGTTCTAG
 CGCCTCTAGTCGAATTAGGTCTCTAAACCAACCCACCTCTGGCCTTTCACGCGCCCCAAGTGGGTTCTAG

 2250 2260 2270 2280 2290 2300 2310 2320
 ACGCTGTTCCCCAGCATTGCTGGCATTAAACTTCACACAGTCTAGAGCCTTCTGTGTTCTAGATTCGTTGTG
 ACGCTGTTCCCCAGCATTGCTGGCATTAAACTTCACACAGTCTAGAGCCTTCTGTGTTCTAGATTCGTTGTG

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FIGURE 7 (CONT)

2330 2340 2350 2360 2370 2380 2390 2400
CTGAGCCCTGGTTTTCCCCACCCCCAACATCTGGATGCTGTTCAACTCTTCCCAGAAACCCACTCCGTGTGGGG
.....
CTGAGCCCTGGTTTTCCCCACCCCCAACATCTGGATGCTGTTCAACTCTTCCCAGAAACCCACTCCGTGTGGGG

2410 2420 2430 2440 2450 2460 2470
TTCTAGACTCTATCTTGGTAGTTTATGCCTTCTCTCCCTAGACCACGTTGGGAGAAATAGTCTCATGAGATTGC
.....
TTCTAGACTCTATCTTGGTAGTTTATGCCTTCTCTCCCTAGACCACGTTGGGAGAAATAGTCTCATGAGATTGC

2480 2490 2500 2510 2520 2530 2540 2550
CTGCTCCAGACTAAGATTCAGATCAGCTCTCTGCATCCTCAAGGGCCCTCCTACCTCCACTTCAGTTGTAGAA
.....
CTGCTCCAGACTAAGATTCAGATCAGCTCTCTGCATCCTCAAGGGCCCTCCTACCTCCACTTCAGTTGTAGAA

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FIGURE 8

M13977 Human clone 28
 Z15114

-190 -180 -170 -160 -150 -140

CCTTGGAGCCGGCGCCCCGGGTGCCGCTCCCTGCCTGGCGCTCCGCACCTG

M13977 Human clone 28
 Z15114

-130 -120 -110 -100 -90

GAGGTGCCTGCCCTCTCCTGCCACCTCGGAATTCCCTGTGGCTCCTTGATCC
CCTTGATCC

M13977 Human clone 28
 Z15114

-80 -70 -60 -50 -40 -30

TTGGAGTCTCCAGCTCCTCTCCCTCACCTGTTCCCCAAGAAAGGCAGGATCCT
TTGGAGTCTCCAGCTCCTCTCCCTCACCTGTTCCCCAAGAAAGGCAGGATCCT

M13977 Human clone 28
 Z15114

-20 -10 1 10 20 30

GGTCCCTGCTACGTTCTGGGGCCATGGCTGGCTGGGCCCCGGCGTAGGCGATTCA
GGTCCCTGCTACGTTCTGGGGCCATGGCTGGCTGGGCCCCGGCGTAGGCGATTCA

Start codon

M13977 Human clone 28
 Z15114

40 50 60 70 80

GAGGGGGGACCCGGCCCTGTTCTGCAGAAAGGGGCTCTGAGGCAGAAAGGTGGTC
GAGGGGGGACCCGGCCCTGTTCTGCAGAAAGGGGCTCTGAGGCAGAAAGGTGGTC

M13977 Human clone 28
 Z15114

90 100 110 120 130 140

CACGAAGTCAAGAGCCACAAGTTCACCGCTCGCTTCTCAAGCAGCCCACCTCTGC
CACGAAGTCAAGAGCCACAAGTTCACCGCTCGCTTCTCAAGCAGCCCACCTCTGC

M13977 Human clone 28
 Z15114

150 160 170 180 190 200

AGCCACTGCACCGACTTCATCTGGGTATCGAAAGCAGGGCTGCAATGTCAAGTC
AGCCACTGCACCGACTTCATCTGGGTATCGAAAGCAGGGCTGCAATGTCAAGTC

M13977 Human clone 28
 Z15114

210 220 230 240 250 260

TGCAGCTTTGTGGTTCATGACGATGCCACGAATTGACCTCGAGTGTCCAGGC
TGCAGCTTTGTGGTTCATGACGATGCCACGAATTGACCTCGAGTGTCCAGGC

M13977 Human clone 28
 Z15114

270 280 290 300 310

GCTGGGAAGGGCCCCAGACGGACGACCCCGGAACAAACACAAGTCCGCCTGCAT
GCTGGGAAGGGCCCCAGACGGACGACCCCGGAACAAACACAAGTCCGCCTGCAT

M13977 Human clone 28
 Z15114

320 330 340 350 360 370

AGCTACAGCAGCCCCACCTCTGCGACCAACTGTGGCTCCCTCTACGGGCTTGTG
AGCTACAGCAGCCCCACCTCTGCGACCAACTGTGGCTCCCTCTACGGGCTTGTG

M13977 Human clone 28
 Z15114

380 390 400 410 420 430

CACCAGGGCATGAAATGTTCTTGCTGCGAGATGAACGTGCACCGGGCGTGTGCG
CACCAGGGCATGAAATGCTCTGCTGCGAGATGAACGTGCACCGGGCGTGTGCG

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FIGURE 8 (CONT.)

M13977 Human clone 28
Z15114

440 450 460 470 480

TAGCGTGCCTCTCTGTGCGGTGTGGACCAACCGAGCGCCGCGGGCGCCCTGCAGCT
TAGCGTGCCTCCCTGTGCGGTGTGGACCAACCGAGCGCCGCGGGCGCCCTGCAGCT
TGCAGCT

M13977 Human clone 28
Z15114

490 500 510 520 530 540

GGAGATCCGGCTCCCACAGCAGATGAGATCCACGTAACGTAACTGTTGGGAGGGCCCGTAA
GGAGATCCGGCTCCCACAGCAGATGAGATCCACGTAACGTAACTGTTGGGAGGGCCCGTAA
GGAGATCCGGCTCCCACAGCAGATGAGATCCACGTAACGTAACTGTTGGGAGGGCCCGTAA

M13977 Human clone 28
Z15114

550 560 570 580 590 600

CCTAATTCTATGGACCCCAATGGTCTCTCTGATCCCTATGTGAAACTGAAGCTCAT
CCTAATTCTATGGACCCCAACGGTCTCTCTGATCCCTATGTGAAACTGAAGCTCAT
CCTAATTCTATGGACCCCAATGGTCTCTCTGATCCCTATGTGAAACTGAAGCTCAT

M13977 Human clone 28
Z15114

610 620 630 640 650

CCCAGACCCCTCGGAACCTGACGAAACAGAAGACCCGAACGGTGAAGGCCACGCTAAA
CCCAGACCCCTCGGAACCTGACGAAACAGAAGACCCGAACGGTGAAGGCCACGCTAAA
CCCAGACCCCTCGGAACCTGACGAAACAGAAGACCCGAACGGTGAAGGCCACGCTAAA

M13977 Human clone 28
Z15114

660 670 680 690 700 710

CCCTGTGTGGATGAGACCTTGTGTTAACCTGAAGCCAGGGGATGTGGAGCGCCG
CCCTGTGTGGATGAGACCTTGTGTTAACCTGAAGCCAGGGGATGTGGAGCGCCG
CCCTGTGTGGATGAGACCTTGTGTTAACCTGAAGCCAGGGGATGTGGAGCGCCG

M13977 Human clone 28
Z15114

720 730 740 750 760 770

GCTCAGCGTGGAGGTGTGGGACTGGGACCGGACCTCCCGCAACGACTTCATGGGGC
GCTCAGCGTGGAGGTGTGGGACTGGGACCGGACCTCCCGCAACGACTTCATGGGGC
GCTCAGCGTGGAGGTGTGGGACTGGGACCGGACCTCCCGCAACGACTTCATGGGGC

M13977 Human clone 28
Z15114

780 790 800 810 820 830

CATGCTTTGGCGTCTCGAGCTGCTCAAGGCGCCCGTGGATGGCTGGTACAAGTT
CATGCTTTGGCGTCTCGAGCTGCTCAAGGCGCCCGTGGATGGCTGGTACAAGTT
CATGCTTTGGCGTCTCGAGCTGCTCAAGGCGCCCGTGGATGGCTGGTACAAGTT

M13977 Human clone 28
Z15114

840 850 860 870 880

ACTGAACCAGGAGGAGGGCAGTATTACAATGTGCCGGTGGCTGATGCTGACAACCTG
ACTGAACCAGGAGGAGGGCAGTATTACAATGTGCCGGTGGCCATGCTGACAACCTG
ACTGAACCAGGAGGAGGGCAGTATTACAATGTGCCGGTGGCCATGCTGACAACCTG

M13977 Human clone 28
Z15114

890 900 910 920 930 940

CAGCTCCTCCAGAAGTTGAGGCTTGTAACTACCCCTGGAAATTGTATGA
CAGCTCCTCCAGAAGTTGAGGCTTGTAACTACCCCTGGAAATTGTATGAAGCGGGT
CAGCTCCTCCAGAAGTTGAGGCTTGTAACTACCCCTGGAAATTGTATGAAGCGGGT

M13977 Human clone 28
Z15114

950 960 970 980 990 1000

GC GGATGGGCCCTTCCCTCCATCCCCCTCCCTAGTCCCACCGACCC
GC GGATGGGCCCTTCCCTCCATCCCCCTCCCTAGTCCCACCGACCC

M13977 Human clone 28
Z15114

1010 1020 1030 1040 1050

CAAGCGCTGCTTCTCGGGCGAGTCCAGGACGCCCTGCACATCTCCGACTTCAGCTT
CAAGCGCTGCTTCTCGGGCGAGTCCAGGACGCCCTGCACATCTCCGACTTCAGCTT

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FIGURE 8 (CONT)

M13977 Human clone 28
 Z15114

1060	1070	1080	1090	1100	1110
CCTCATGGTTCTAGGAAAAGGCAGTTTGGGAAGGTGATGCTGGCCGAGCGCAGGGG					
CCTCATGGTTCTAGGAAAAGGCAGTTTGGGAAGGTGATGCTGGCCGAGCGCAGGGG					

M13977 Human clone 28
 Z15114

1120	1130	1140	1150	1160	1170
CTCTGATGAGCTCTACGCCATCAAGATCTTGAAGGACGTGATCGTCAGGACGA					
CTCTGATGAGCTCTACGCCATCAAGATCTTGAAGGACGTGATCGTCAGGACGA					

M13977 Human clone 28
 Z15114

1180	1190	1200	1210	1220	
CGATGTGGACTGCACGCTGGTGGAGAAACGTGTGCTGGCGCTGGGGGGCGGGGTCC					
CGATGTGGACTGCACGCTGGTGGAGAAACGTGTGCTGGCGCTGGGGGGCGGGGTCC					

M13977 Human clone 28
 Z15114

1230	1240	1250	1260	1270	1280
TGGCGGCCGGCCCCACTTCCTCACCCAGCTCCACTCCACCTTCAGACCCGGACC					
TGGCGGCCGGCCCCACTTCCTCACCCAGCTCCACTCCACCTTCAGACCCGGACC					

M13977 Human clone 28
 Z15114

1290	1300	1310	1320	1330	1340
GCCTGTATTCGTGATGGAGTACGTACCGGGGGAGACTTGATGTACCACTTCAC					
GCCTGTATTCGTGATGGAGTACGTACCGGGGGAGACTTGATGTACCACTTCAC					

M13977 Human clone 28
 Z15114

1350	1360	1370	1380	1390	1400
AGCTGGCAAGTTAAGGAGCCCCATGCAGCGTTCTACGGCGAGAAATCGCTATCG					
AGCTGGCAAGTTAAGGAGCCCCATGCAGCGTTCTACGGCGAGAAATCGCTATCG					

M13977 Human clone 28
 Z15114

1410	1420	1430	1440	1450	
GCCTCTTCTTCCTTACAATCAGGGCATCATCTACAGGGACCTGAAGCTGGACAATG					
GCCTCTTCTTCCTTACAATCAGGGCATCATCTACAGGGACCTGAAGCTGGACAATG					

M13977 Human clone 28
 Z15114

1460	1470	1480	1490	1500	1510
TGATGCTGGATGCTGAGGGACACATCAAGATCACTGACTTTGGCATGTGTAAGGAGA					
TGATGCTGGATGCTGAGGGACACATCAAGATCACTGACTTTGGCATGTGTAAGGAGA					

M13977 Human clone 28
 Z15114

1520	1530	1540	1550	1560	1570
ACGTCTTCCCCGGGACGACAACCGCACCTCTGCGGGACCCCGGACTACATAGCCC					
ACGTCTTCCCCGGGACGACAACCGCACCTCTGCGGGACCCCGGACTACATAGCCC					

M13977 Human clone 28
 Z15114

1580	1590	1600	1610	1620	
CGGAGATCATTGCCTACCAGCCCTATGGGAAGTCTGTCGATTGGTGGCCTTGGAG					
CGGAGATCATTGCCTACCAGCCCTATGGGAAGTCTGTCGATTGGTGGCCTTGGAG					

M13977 Human clone 28
 Z15114

1630	1640	1650	1660	1670	1680
TTCTGCTGTATGAGATGTTGGCAGGACAGCCTCCCTCGATGGGGAGGACGAGGAGG					
TTCTGCTGTATGAGATGTTGGCAGGACAGCCTCCCTCGATGGGGAGGACGAGGAGG					

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FIGURE 8 (CONT.)

M13977 Human clone 28 Z15114	1690 1700 1710 1720 1730 1740	AGCTGTTTCAGGCCATCATGGAACAAACTGTCACCTACCCCAAGTCGCTTCCGGG AGCTGTTTCAGGCCATCATGGAACAAACTGTCACCTACCCCAAGTCGCTTCCGGG
M13977 Human clone 28 Z15114	1750 1760 1770 1780 1790	AAGCCGTGGCCATCTGCAAGGGTTCTGACCAAGCACCAGGGAAAGCGCCCTGGGCT AAGCCGTGGCCATCTGCAAGGGTTCTGACCAAGCACCAGGGAAAGCGCCCTGGGCT
M13977 Human clone 28 Z15114	1800 1810 1820 1830 1840 1850	CAGGGCCTGATGGGGAACCTACCATCCGTGCACATGGCTTTCCGCTGGATTGACT CAGGGCCTGATGGGGAACCTACCATCCGTGCACATGGCTTTCCGCTGGATTGACT
M13977 Human clone 28 Z15114	1860 1870 1890 1900 2000 2010	GGGAGCGGCTGGAACGATTGGAGATCCCGCCTCCCTTCAGACCCCCGCCCCGTGGCC GGGAGCGGCTGGAACGATTGGAGATCCCGCCTCCCTTCAGACCCCCGCCCCGTGGCC
M13977 Human clone 28 Z15114	2020 2030 2040 2050 2060 2070	GCAGCGGCGAGAACCTTGACAAGTTCTTCACGCGGGCGGCCAGCGCTGACCCCTC GCAGCGGCGAGAACCTTGACAAGTTCTTCACGCGGGCGGCCAGCGCTGACCCCTC
M13977 Human clone 28 Z15114	2080 2090 2100 2110 2120	CAGACCGCCTAGTCCTGGCCAGCAGTCACGACCAAGGCCGATTTCAGGGCTTCACCTACG CAGACCGCCTAGTCCTGGCCAGCAGTCACGACCAAGGCCGATTTCAGGGCTTCACCTACG
M13977 Human clone 28 Z15114	2130 2140 2150 2160 2170 2180	TGAACCCCGACTTCGTGCACCCGGATGCCCGCAGCCCCACCAAGCCCAGTGCCTGTGC TGAACCCCGACTTCGTGCACCCGGATGCCCGCAGCCCCACCAAGCCCAGTGCCTGTGC
M13977 Human clone 28 Z15114	2190 2200 2210 2220 2230 2240	CCGTCATGTAATCTCAC CCGTCATGTAATCTCACCCGCCACTAGGTGTCCCCAACGTCCCCCTCCGCCGTGC
M13977 Human clone 28 Z15114	2250 2260 2270 2280 2290	Stop codon CGCGGGCAGCCCCACTTCACCCCAACTTCACCAACCCCTGTCCCATTCTAGATCCT
M13977 Human clone 28 Z15114	2300 2310 2320 2330 2340 2350	GCACCCCAAGCATTCCAGCTCTGCCCGCGGGTTCTAGACGCCCTCCCAAGCGTTC
M13977 Human clone 28 Z15114	2360 2370 2380 2390 2400 2410	CTGGCCTCTGAACCTCCATAAGCCTCTACAGCCGTCCCGCGTTCAAGACTTGAGCG

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FIGURE 9

-140 -130 -120 -110 -100 -90 -80 -70
 TGCTTTCTGCCCTGCGCTGCGCACCGTTAGTGCCCTGCCCTGTCCCTCCGATCTCAGAGTCTCGGGAGTGCCCTA

 CCTTCCGATCTCAGAGTCTCGGGAGTGCCCTA

-60 -50 -40 -30 -20 -10 1 10
 TCGCCGTCCACCTGTTCTCAGAAAAAGGCCAGCTCGTATCCCTGCTGCGTTCTGGGGCCATGGCGGGCTGG

 TCGCCGTCCACCTGTTCTCAGAAAAAGGCCAGCTCGTATCCCTGCTGCGTTCTGGGGCCATGGCGGGCTGG
 Start Codon

20 30 40 50 60 70 80
 GTCCCTGGCGGGGGCGACTCAGAAGGGGGACCCCGACCCCTGTTTGAGAAAGGGGGCGCTGAGGCAGAAGGTGGTC

 GTCCCTGGCGGGGGCGACTCAGAAGGGGGACCCCGACCCCTGTTTGAGAAAGGGGGCGCTGAGGCAGAAGGTGGTC

90 100 110 120 130 140 150 160
 CACGAGGTGAAGAGCCACAAGTTCACCGCTCGTTCTCAAGCAGCCAACCTCTGCAGTCAGTCACTGTACCGACTTCAT

 CACGAGGTGAAGAGCCACAAGTTCACCGCTCGTTCTCAAGCAGCCAACCTCTGCAGTCAGTCACTGTACCGACTTCAT

170 180 190 200 210 220 230 240
 CTGGGGCATTGAAAGCAGGGCCTGCAATGTCAGTCTGCAGCTTGTGGTTCACCGCCGATGCCACGAATTGTGA

 CTGGGGCATTGAAAGCAGGGCCTGCAATGTCAGTCTGCAGCTTGTGGTTCACCGCCGATGCCACGAATTGTGA

250 260 270 280 290 300 310 320
 CCTTCGAGTGTCAGGCCTGGAAAGGGCCCCAGACGGACGACCCCTCGAACACAAGCACAAGTTCCGTCTGCACAGC

 CCTTCGAGTGTCAGGCCTGGAAAGGGCCCCAGACGGACGACCCCTCGAACACAAGCACAAGTTCCGTCTGCACAGC

330 340 350 360 370 380 390
 TACAGCAGTCCCACCTCTCGGACCACTGTGGTCCCTCTACGGGCTGGTGCACCAAGGGCATGAAATGTTCTG

 TACAGCAGTCCCACCTCTCGGACCACTGTGGTCCCTCTACGGGCTGGTGCACCAAGGGCATGAAATGTTCTG

400 410 420 430 440 450 460 470
 TTGCGAAATGAATGTGCACCGACGCTGTGTGCGCAGCGTGCCTCCCTTGGGGCTGGACCATAACAGAGGCCGTG

 TTGCGAAATGAATGTGCACCGACGCTGTGTGCGCAGCGTGCCTCCCTTGGGGCTGGACCATAACAGAGGCCGTG

480 490 500 510 520 530 540 550
 GACGTCTGCAACTGGAAATCCGGGCTCCACATCAGATGAGATCCATATTACTGTGGGTGAGGCCCGAACCTCATT

 GACGTCTGCAACTGGAAATCCGGGCTCCACATCAGATGAGATCCATATTACTGTGGGTGAGGCCCGAACCTCATT

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FIGURE 9 (CONT)

560 570 580 590 600 610 620
 CCTATGGACCCCAATGGCCTGTCTGATCCCTATGTGAAACTGAAGCTCATCCCGACCCCTCGAACCTGACAAAACA
 CCTATGGACCCCAATGGCCTGTCTGATCCCTATGTGAAACTGAAGCTCATCCCGACCCCTCGAACCTGACAAAACA

 630 640 650 660 670 680 690 700
 GAAGACAAAGACCGTGAAAGCCACACTGAATCCCGTGTGGAACGAGACCTTCGTGTTCAACCTGAAGCCGGGGATG
 GAAGACAAAGACCGTGAAAGCCACACTGAATCCCGTGTGGAACGAGACCTTCGTGTTCAACCTGAAGCCGGGGATG

 710 720 730 740 750 760 770 780
 TGGAGCGCCGGCTCAGTGTGGAGGTGTGGGATTGGGATAGGACATCCCGAAATGACTTCATGGGTGCCATGTCCTTT
 TGGAGCGCCGGCTCAGTGTGGAGGTGTGGGATTGGGATAGGACATCCCGAAATGACTTCATGGGTGCCATGTCCTTT

 790 800 810 820 830 840 850
 GGTGTCTCAGAGCTACTCAAGGCTCCTGTGGATGGATGGTACAAGTTACTGAACCAGGAGGGCGAGTATTACAA
 GGTGTCTCAGAGCTACTCAAGGCTCCTGTGGATGGATGGTACAAGTTACTGAACCAGTGGAGGGCGAGTATTACAA
 Stop Codon

 860 870 880 890 900 910 920 930
 TGTACCGGTGGCCGATGCTGACAACACTGCAGCCTCCTCCAGAAGTTGAGGCCTGTAATTACCCCTTGGAAATTGTATG
 TGTACCGGTGGCCGATGCTGACAACACTGCAGCCTCCTCCAGAAGTTGAGGCCTGTAATTACCCCTTGGAAATTGTATG

 940 950 960 970 980 990 1000 1010
 AGAGAGTGCAGGATGGGCCCTTCCCTCTCCATTCCCTCCATCCCCAGTCCACGGACTCCAAGAGATGCTTC
 AGAGAGTGCAGGATGGGCCCTTCCCTCTCCATTCCCTCCATCCCCAGTCCACGGACTCCAAGAGATGCTTC

 1020 1030 1040 1050 1060 1070 1080
 TTGGTGCCAGCCAGGACGCCTGCATATCTCTGACTTCAGCTCCTCATGGTTCTAGGGAAAGGCAGTTTGGAA
 TTGGTGCCAGCCAGGACGCCTGCATATCTCTGACTTCAGCTCCTCATGGTTCTAGGGAAAGGCAGTTTGGAA

 1090 1100 1110 1120 1130 1140 1150 1160
 GGTGATGCTGGCAGAGCGCAGAGGATCCGATGAACTCTATGCCATCAAGATACTGAAAAAGACGTCATTGTCCAGG
 GGTGATGCTGGCAGAGCGCAGAGGATCCGATGAACTCTATGCCATCAAGATACTGAAAAAGACGTCATTGTCCAGG

 1170 1180 1190 1200 1210 1220 1230 1240
 ATGATGATGTAGACTGCACCCCTGTGGAGAAGCGTGTGCTGGCATTGGGAGGCCGAGGTCTGGAGGCCGGCACAC
 ATGATGATGTAGACTGCACCCCTGTGGAGAAGCGTGTGCTGGCATTGGGAGGCCGAGGTCTGGAGGCCGGCACAC

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FIGURE 9 (CONT)

1250 1260 1270 1280 1290 1300 1310 1320
 TTTCTCACACAACCTTCATTCCACCTTCAGACTCCGGACCGCCTGTATTTGTGATGGAGTACGTCACTGGGGCGA
 TTTCTCACACAACCTTCATTCCACCTTCAGACTCCGGACCGCCTGTATTTGTGATGGAGTACGTCACTGGGGCGA

 1330 1340 1350 1360 1370 1380 1390
 TTTAATGTACCACATTCACTGGCAAGTTAAGGAGCCCCACGCAGCATTCTATGCCGGAAATGCCATAG
 TTTAATGTACCACATTCACTGGCAAGTTAAGGAGCCCCACGCAGCATTCTATGCCGGAAATGCCATAG

 1400 1410 1420 1430 1440 1450 1460 1470
 GCCTCTTCTTCTTCACAACCAGGGCATCATCTACAGGGACCTCAAGTTGATAATGTGATGCTGGATGCTGAAGGA
 GCCTCTTCTTCTTCACAACCAGGGCATCATCTACAGGGACCTCAAGTTGATAATGTGATGCTGGATGCTGAAGGA

 1480 1490 1500 1510 1520 1530 1540 1550
 CACATCAAGATCACAGACTTCGGCATGTGTAAAGAGAATGTCTCCCTGGTCCACAACCCGCACCTCTGTGGGAC
 CACATCAAGATCACAGACTTCGGCATGTGTAAAGAGAATGTCTCCCTGGTCCACAACCCGCACCTCTGTGGGAC

 1560 1570 1580 1590 1600 1610 1620
 CCCAGACTACATAGCACCTGAGATCATTGCCTATCAGCCCTATGGAAAGTCTGTCGACTGGTGGCCTTGGAGTCC
 CCCAGACTACATAGCACCTGAGATCATTGCCTATCAGCCCTATGGAAAGTCTGTCGACTGGTGGCCTTGGAGTCC

 1630 1640 1650 1660 1670 1680 1690 1700
 TGCTGTATGAGATGTTGGCAGGACAGCCACCCCTTGATGGGGAAAGATGAGGGAGGAGCTGTTCAAGCCATCATGGAA
 TGCTGTATGAGATGTTGGCAGGACAGCCACCCCTTGATGGGGAAAGATGAGGGAGGAGCTGTTCAAGCCATCATGGAA

 1710 1720 1730 1740 1750 1760 1770 1780
 CAAACTGTCACCTATCCCAAGTCACCTTCCGGAAAGCTGTGCCATCTGCAAGGGGTTCTGACCAAGCACCAGG
 CAAACTGTCACCTATCCCAAGTCACCTTCCGGAAAGCTGTGCCATCTGCAAGGGGTTCTGACCAAGCACCAGG

 1790 1800 1810 1820 1830 1840 1850
 AAAGCGCCTGGGCTCAGGGCCAGATGGGGAAACCCACCATCCGGCTCATGGCTTTTCCGTTGGATCGATTGGGAGA
 AAAGCGCCTGGGCTCAGGGCCAGATGGGGAAACCCACCATCCGGCTCATGGCTTTTCCGTTGGATCGATTGGGAGA

 1860 1870 1880 1890 1900 1910 1920 1930
 GGTTGGAGAGACTGGAAATTGCGCCTCTTTAGACCACTGGCCAGCAGCGGGAAAACCTTGACAAAGTTC
 GGTTGGAGAGACTGGAAATTGCGCCTCTTTAGACCACTGGCCAGCAGCGGGAAAACCTTGACAAAGTTC

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FIGURE 9 (CONT)

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FIGURE 10

10 20 30 40 50 60 70
 MAGLGPGGGDSEGGPRPLFCRKGALRQKVHEVKSHFTARFFKQPTFCSHCTDFIWIWGIGKQGLQCQVCSFVVRRC
 MAGLGPGGGDSEGGPRPLFCRKGALRQKVHEVKSHFTARFFKQPTFCSHCTDFIWIWGIGKQGLQCQVCSFVVRRC

 80 90 100 110 120 130 140 150
 HEFVTFECPGAGKGPQTDDPRNKHKFRLHSYSSPTFCDHCGSLLYGLVHQGMKCSCEMNVHRRCVRSVPSLCGVDH
 HEFVTFECPGAGKGPQTDDPRNKHKFRLHSYSSPTFCDHCGSLLYGLVHQGMKCSCEMNVHRRCVRSVPSLCGVDH

 160 170 180 190 200 210 220 230
 TERRGRLQLEIRAPTSDEIHIITVGEARNLIPMDPNGLSDPYVKLKLIPDPRNLTKQKTKTVKATLNPVWNETFVFNL
 TERRGRLQLEIRAPTSDEIHIITVGEARNLIPMDPNGLSDPYVKLKLIPDPRNLTKQKTKTVKATLNPVWNETFVFNL
 240 250 260 270 280
 KPGDVERRLSVEVWDWDRTSRNDFMGAMSFGVSELLKAPVDGWYKLLNQ
 KPGDVERRLSVEVWDWDRTSRNDFMGAMSFGVSELLKAPVDGWYKLLNQEEGEYYNVPADADNCSSLQKFEACNYP

 310 320 330 340 350 360 370 380
 LEIYERVRMGPSSSPIPSPTDSKRCFFGASPGRHLHISDFSFLMVLGKGSFGKVMLAERRGSDELYAIKILKKD

 390 400 410 420 430 440 450 460
 VIVQDDDVDCILVEKRVIALGGRGPGGRPHFLTQLHSTFQTPDRLYFVMEYVTGGDILMYHIQQLGKFKEPHAAFYAA

 470 480 490 500 510 520 530
 EIAIGLFFLHNQGIIYRDLKLDNVMLDAEGHIKITDFGMCKENVFPGSTRTFCGTPDYIAPEIIAYQPYGKSVVDWW

 540 550 560 570 580 590 600 610
 SFGVLLYEMLAGQPPFDGEDEEELFOAIMEQTVTYPKSLSREAVAICKGFLTKHPGKRLGSGPDGEPTIRAHGFFRW

 620 630 640 650 660 670 680 690
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 VPVM

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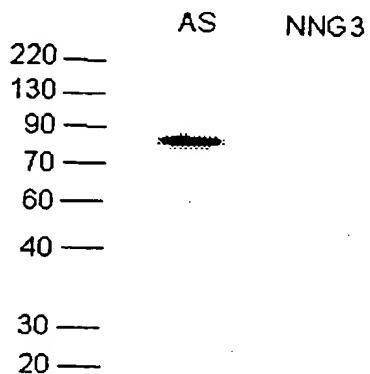
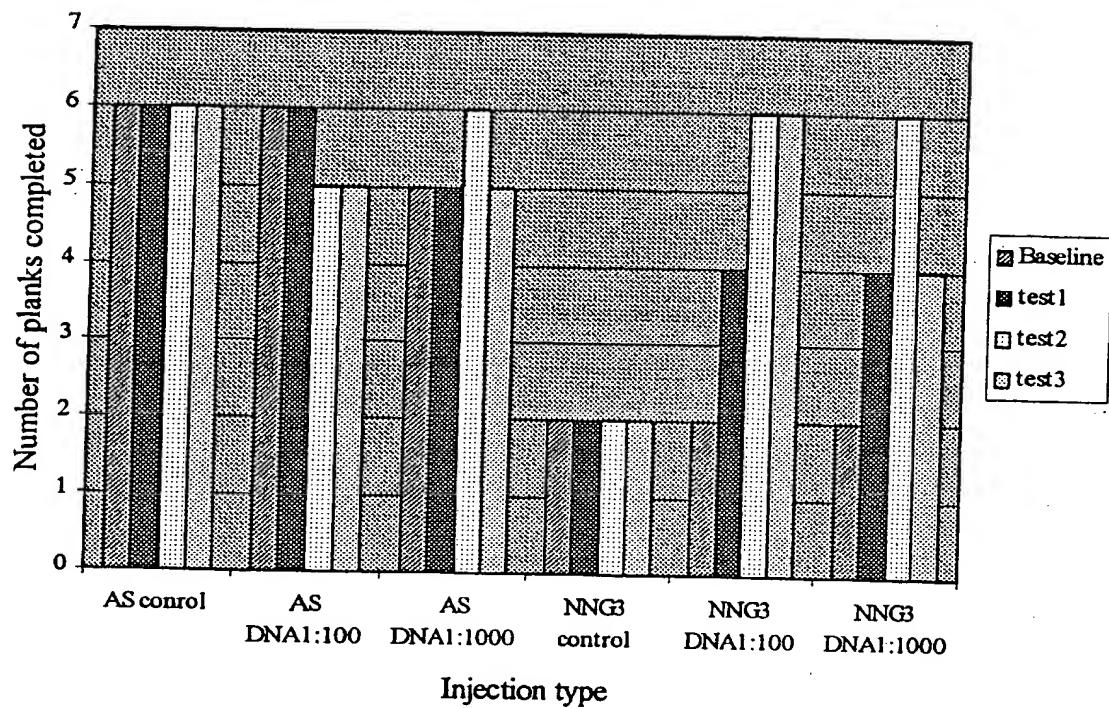
FIGURE 11

FIGURE 12
Inclined Ramp Test - experiment 1



Inclined Ramp Test - experiment 2

